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SEQUENCE LISTING

<110> Weiner, Richard I.
Martial, Joseph A.
Struman, Ingrid
Taylor, Robert
Bentzien, Frauke

<120> Novel Antiangiogenic Peptide Agents and Their Therapeutic and Diagnostic Use

<130> UCSF-018/02US

<140> 09/819,094
<141> 2001-03-27

<150> 09/076,675
<151> 1998-05-12

<150> 60/046,394
<151> 1997-05-12

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35 40 45

Arg Gly Phe Ile Thr Lys Ala Ile Asn Ser Cys His Thr Ser Ser Leu
50 55 60

Ala Thr Pro Glu Asp Lys Glu Gln Ala Gln Gln Met Asn Gln Lys Asp
65 70 75 80

Phe Leu Ser Leu Ile Val Ser Ile Leu Arg Ser Trp Asn Glu Pro Leu
85 90 95

Tyr His Leu Val Thr Glu Val Arg Gly Met Gln Glu Ala Pro Glu Ala
100 105 110

Ile Leu Ser Lys Ala Val Glu Ile Glu Glu Gln Thr Lys Arg Leu Leu
115 120 125

Glu Gly Met Glu Leu Ile Val Ser Gln Val His Pro Glu Thr Lys Glu
130 135 140

Asn Glu Ile Tyr Pro Val Trp Ser Gly Leu Pro Ser Leu Gln Met Ala
145 150 155 160

Asp Glu Glu Ser Arg Leu Ser Ala Tyr Tyr Asn Leu Leu His Cys Leu
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180 185 190

Arg Ile Ile His Asn Asn Asn Cys
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Leu Ser Ser Glu Met Phe Ser Glu Phe Asp Lys Arg Tyr Thr His Gly
        35                  40                  45

Arg Gly Phe Ile Thr Lys Ala Ile Asn Ser Ser His Thr Ser Ser Leu
    50                  55                  60

Ala Thr Pro Glu Asp Lys Glu Gln Ala Gln Gln Met Asn Gln Lys Asp
65                  70                  75                  80

Phe Leu Ser Leu Ile Val Ser Ile Leu Arg Ser Trp Asn Glu Pro Leu
                85                  90                  95

Tyr His Leu Val Thr Glu Val Arg Gly Met Gln Glu Ala Pro Glu Ala
            100                 105                 110

Ile Leu Ser Lys Ala Val Glu Ile Glu Glu Gln Thr
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Arg Asp Leu Phe Asp Arg Ala Val Val Leu Ser His Tyr Ile His Asn
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Leu Ser Ser Glu Met Phe Ser Glu Phe Asp Lys Arg Tyr Thr His Gly
        35                  40                  45

Arg Gly Phe Ile Thr Lys Ala Ile Asn Ser Ser His Thr Ser Ser Leu
    50                  55                  60

Ala Thr Pro Glu Asp Lys Glu Gln Ala Gln Gln Met Asn Gln Lys Asp
65                  70                  75                  80

Phe Leu Ser Leu Ile Val Ser Ile Leu Arg Ser Trp Asn Glu Pro Leu
                85                  90                  95

Tyr His Leu Val Thr Glu Val Arg Gly Met Gln Glu Ala Pro Glu Ala
            100                 105                 110

Ile Leu Ser Lys Ala Val Glu Ile Glu Glu Gln Thr Lys Arg Leu Leu
        115                 120                 125
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             20                  25                  30

Leu Ser Ser Glu Met Phe Ser Glu Phe Asp Lys Arg Tyr Thr His Gly
         35                  40                  45

Arg Gly Phe Ile Thr Lys Ala Ile Asn Ser Ser His Thr Ser Ser Leu
     50                  55                  60

Ala Thr Pro Glu Asp Lys Glu Gln Ala Gln Gln Met Asn Gln Lys Asp
 65                  70                  75                  80

Phe Leu Ser Leu Ile Val Ser Ile Leu Arg Ser Trp Asn Glu Pro Leu
                 85                  90                  95

Tyr His Leu Val Thr Glu Val Arg Gly Met Gln Glu Ala Pro Glu Ala
            100                 105                 110

Ile Leu Ser Lys Ala Val Glu Ile Glu Glu Gln Thr Lys Arg Leu Leu
        115                 120                 125

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Glu Glu Thr Tyr Ile Pro Lys Asp Gln Lys Tyr Ser Phe Leu His Asp
35 40 45

Ser Gln Thr Ser Phe Cys Phe Ser Asp Ser Ile Pro Thr Pro Ser Asn
50 55 60

Met Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
65 70 75 80

Leu Leu Leu Ile Glu Ser Trp Leu Glu Pro Val Arg Phe Leu Arg Ser
85 90 95

Met Phe Ala Asn Asn Leu Val Tyr Asp Thr Ser Asp Ser Asp Asp Tyr
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His Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg
115 120 125

Leu Glu Asp Gly Ser Arg Arg Thr Gly Gln Ile Leu Lys Gln Thr Tyr
130 135 140

Ser Lys Phe Asp Thr Asn Ser His Asn His Asp Ala Leu Leu Lys Asn
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Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr
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Phe Leu Arg Met Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe
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<210> 18
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<213> Homo sapiens

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Glu Glu Thr Tyr Ile Pro Lys Asp Gln Lys Tyr Ser Phe Leu His Asp
         35                  40                  45

Ser Gln Thr Ser Phe Ser Phe Ser Asp Ser Ile Pro Thr Pro Ser Asn
     50                  55                  60

Met Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
 65                  70                  75                  80

Leu Leu Leu Ile Glu Ser Trp Leu Glu Pro Val Arg Phe Leu Arg Ser
                 85                  90                  95

Met Phe Ala Asn Asn Leu Val Tyr Asp Thr Ser Asp Ser Asp Asp Tyr
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His Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg
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Leu Glu Asp Gly Ser Pro Arg
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Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe
20 25 30

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Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn
     50                  55                  60

Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
 65                  70                  75                  80

Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser
                 85                  90                  95

Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr
            100                 105                 110

Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg
        115                 120                 125

Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr
    130                 135                 140

Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn
145                 150                 155                 160

Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr
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Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe
            20                  25                  30

Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn
        35                  40                  45

Pro Gln Thr Ser Leu Ser Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn
    50                  55                  60
```

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Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
 65                  70                  75                  80

Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser
                85                  90                  95

Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr
            100                 105                 110

Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg
        115                 120                 125

Leu Glu Asp Gly Ser Pro
    130
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<210> 25
<211> 579
<212> DNA
<213> Homo sapiens

<400> 25
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ctgtaccagc tggcatatga cacctatcag gagtttgaag aagcctatat cctgaaggag 120
cagaagtatt cattcctgca gaacccccag acctccctct gcttctcaga gtctattcca 180
acaccttcca acagggtgaa aacgcagcag aaatctaacc tagagctgct ccgcatctcc 240
ctgctgctca tccagtcatg gctggagccc gtgcagctcc tcaggagcgt cttcgccaac 300
agcctggtgt atggcgcctc ggacagcaac gtctatcgcc acctgaagga cctagaggaa 360
ggcatccaaa cgctgatgtg gaggctggaa gatggcagcc cccggactgg gcagatcttc 420
aatcagtcct acagcaagtt tgacacaaaa tcgcacaacg atgacgcact gctcaagaac 480
tacgggctgc tctactgctt caggaaggac atggacaagg tcgagacatt cctgcgcatc 540
gtgcagtgcc gctctgtgga gggcagctgt ggcttctag   579

<210> 26
<211> 579
<212> DNA
<213> Homo sapiens

<400> 26
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cagaagtatt cattcctgca gaacccccag acctccctct gcttctcaga gtctattcca 180
acaccttcca acagggtgaa aacgcagcag aaatctaacc tagagctgct ccgcatctcc 240
ctgctgctca tccagtcatg gctggagccc gtgcagctcc tcaggagcgt cttcgccaac 300
agcctggtgt atggcgcctc ggacagcaac gtctatcgcc acctgaagga cctagaggaa 360
ggcatccaaa cgctgatgtg gaggctggaa gatggcagcc cccggactgg gcagatcttc 420
aatcagtcct acagcaagtt tgacacaaaa tcgcacaacg atgacgcact gctcaagaac 480
tacgggctgc tctactgctt caggaaggac atggacaagg tcgagacatt cctgcgcatc 540
gtgcagtgcc gctctgtgga gggcagctgt ggcttctag   579

<210> 27

<211> 579
<212> DNA
<213> Homo sapiens

<400> 27
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gacatggtcg accgtatact gtggatagtc ctcaaacttc ttcggatata ggacttcctc 120
gtcttcataa gtaaggacgt cttgggggtc tggagggaga cgaagagtct cagataaggt 180
tgtggaaggt tgtcccactt ttgcgtcgtc tttagattgg atctcgacga ggcgtagagg 240
gacgacgagt aggtcagtac cgacctcggg cacgtcgagg agtcctcgca gaagcggttg 300
tcggaccaca taccgcggag cctgtcgttg cagatagcgg tggacttcct ggatctcctt 360
ccgtaggttt gcgactacac ctccgacctt ctaccgtcgg gggcctgacc cgtctagaag 420
ttagtcagga tgtcgttcaa actgtgtttt agcgtgttgc tactgcgtga cgagttcttg 480
atgcccgacg agatgacgaa gtccttcctg tacctgttcc agctctgtaa ggacgcgtag 540
cacgtcacgg cgagacacct cccgtcgaca ccgaagatc 579

<210> 28
<211> 579
<212> DNA
<213> Homo sapiens

<400> 28
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gtcttcataa gtaaggacgt cttgggggtc tggagggaga cgaagagtct cagataaggt 180
tgtggaaggt tgtcccactt ttgcgtcgtc tttagattgg atctcgacga ggcgtagagg 240
gacgacgagt aggtcagtac cgacctcggg cacgtcgagg agtcctcgca gaagcggttg 300
tcggaccaca taccgcggag cctgtcgttg cagatagcgg tggacttcct ggatctcctt 360
ccgtaggttt gcgactacac ctccgacctt ctaccgtcgg gggcctgacc cgtctagaag 420
ttagtcagga tgtcgttcaa actgtgtttt agcgtgttgc tactgcgtga cgagttcttg 480
atgcccgacg agatgacgaa gtccttcctg tacctgttcc agctctgtaa ggacgcgtag 540
cacgtcacgg cgagacacct cccgtcgaca ccgaagatc 579

<210> 29
<211> 192
<212> PRT
<213> Homo sapiens

<400> 29
Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu
1 5 10 15

Arg Ala Arg Arg Leu Tyr Gln Leu Ala Tyr Asp Thr Tyr Gln Glu Phe
20 25 30

Glu Glu Ala Tyr Ile Leu Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn
35 40 45

Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn
50 55 60

Arg Val Lys Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser

65 70 75 80

Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Leu Leu Arg Ser
85 90 95

Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr
100 105 110

Arg His Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Trp Arg
115 120 125

Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Asn Gln Ser Tyr
130 135 140

Ser Lys Phe Asp Thr Lys Ser His Asn Asp Asp Ala Leu Leu Lys Asn
145 150 155 160

Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr
165 170 175

Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe
180 185 190

<210> 30
<211> 135
<212> PRT
<213> Homo sapiens

<400> 30
Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu
1 5 10 15

Arg Ala Arg Arg Leu Tyr Gln Leu Ala Tyr Asp Thr Tyr Gln Glu Phe
20 25 30

Glu Glu Ala Tyr Ile Leu Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn
35 40 45

Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn
50 55 60

Arg Val Lys Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
65 70 75 80

Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Leu Leu Arg Ser
85 90 95

Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr

100 105 110

Arg His Leu Lys Asp Leu Glú Glu Gly Ile Gln Thr Leu Met Trp Arg
115 120 125

Leu Glu Asp Gly Ser Pro Arg
130 135

<210> 31
<211> 18
<212> DNA
<213> Homo sapiens

<400> 31
cctgaaacca aagaaaat 18

<210> 32
<211> 6
<212> PRT
<213> Homo sapiens

<400> 32
Pro Glu Thr Lys Glu Asn
1 5

<210> 33
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: nucleotide sequence coding for specific cleavage site of the IgA protease

<400> 33
cctagacccc caacacct 18

<210> 34
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:specific cleavage site of the IgA protease

<400> 34
Pro Arg Pro Pro Thr Pro
1 5